



SEQUENCE LISTING

COPY OF PAPERS
ORIGINALLY FILED

<110> Kalchman, Michael
Hayden, Michael R.
Hackam, Abigail
Chopra, Vikramjit
Goldberg, Paul
Nicholson, Donald W.
Vaillancourt, John P.
Rasper, Dita M.

<120> APOPTOSIS MODULATORS THAT INTERACT WITH
THE HUNTINGTON'S DISEASE GENE

<130> MC010PI

<140> 09/701,205

<141> 2000-11-27

<150> PCT/US99/11743

<151> 1999-05-27

<150> 09/085,199

<151> 1998-05-27

<160> 43

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1164

<212> DNA

<213> Human

<220>

<221> misc_feature

<222> (1)...(1164)

<223> n = A,T,C or G

<400> 1

acagctgaca	ccctgcaagg	ccaccgggac	cgcttcatgg	agcagtttac	aaagttgaaa	60
gatctgttct	accgctccag	caacctgcag	tacttcaagc	gggtcattca	gatccccag	120
ctgcctgaga	acccacccaa	cttcctgcga	gcctcagccc	tgtcagaaca	tatcagccct	180
gtggtggtga	tccctgcaga	ggcctcatcc	cccgcacgcg	agccagtcct	agagaaggat	240
gacctcatgg	acatggatgc	ctctcagcag	aattttatttg	acaacaagtt	tgatgacntc	300
tttggcagtt	catccagcag	tgatcccttc	aatttcaaca	gtcaaaatgg	tgtgaacaag	360
gatgagaagg	accacttaat	tgagcgacta	tacagagaga	tcagtggatt	gaaggcacag	420
ctagaaaaca	tgaagactga	gagccagcgg	gttgtgtctg	agctgaaggg	ccacgtcagc	480
gagctggaag	cagatctggc	cgagcagcag	cacctgcggc	agcaggcggc	cgacgactgt	540
gaattcctgc	gggcagaact	ggacgagctc	aggnggcagc	gggaggacac	cgagaaggct	600
cagcggagcc	tgtctgagat	agaaaggaaa	gctcaagcca	atgaacagcg	atatagcaag	660
ctaaaggaga	agtacagcga	gctggttcag	aaccacgctg	acctgctgcg	gaagaatgca	720
gaggtgacca	aacaggtgtc	catggccaga	caagcccagg	tagattttgga	acgagagaaa	780
aaagagctgg	aggatttcgt	ggagcgcctc	agtgaccagg	gccagcggaa	gactcaagaa	840
cagctggaag	ttctagagag	cttgaagcag	gaacttggca	caagccaacg	ggagcttcag	900
gttctgcaag	gcagcctgga	aacttctgcc	cagtcagaag	caaactgggc	agccgagttc	960
gccgagctag	agaaggagcg	ggacagcctg	gtgagtgccg	cagctcatag	ggaggaggaa	1020
ttatctgctc	ttcggaaaga	actgcaggac	actcagctca	aactggccag	cacagaggaa	1080
tctatgtgcc	agcttgccaa	agaccaacga	aaaatgcttc	tggtggggtc	caggaaggct	1140
gcggagcagg	tgatacaaga	cgcg				1164

<210> 2
 <211> 386
 <212> PRT
 <213> Human

<400> 2

```

Thr Ala Asp Thr Leu Gln Gly His Arg Asp Arg Phe Met Glu Gln Phe
 1          5          10          15
Thr Lys Leu Lys Asp Leu Phe Tyr Arg Ser Ser Asn Leu Gln Tyr Phe
          20          25          30
Lys Arg Val Ile Gln Ile Pro Gln Leu Pro Glu Asn Pro Pro Asn Phe
          35          40          45
Leu Arg Ala Ser Ala Leu Ser Glu His Ile Ser Pro Val Val Val Ile
          50          55          60
Pro Ala Glu Ala Ser Ser Pro Asp Ser Glu Pro Val Leu Glu Lys Asp
65          70          75          80
Asp Leu Met Asp Met Asp Ala Ser Gln Gln Asn Leu Phe Asp Asn Lys
          85          90          95
Phe Asp Asp Phe Gly Ser Ser Ser Ser Ser Asp Pro Phe Asn Phe Asn
          100          105          110
Ser Gln Asn Gly Val Asn Lys Asp Glu Lys Asp His Leu Ile Glu Arg
          115          120          125
Leu Tyr Arg Glu Ile Ser Gly Leu Lys Ala Gln Leu Glu Asn Met Lys
130          135          140
Thr Glu Ser Gln Arg Val Val Leu Gln Leu Lys Gly His Val Ser Glu
145          150          155          160
Leu Glu Ala Asp Leu Ala Glu Gln Gln His Leu Arg Gln Gln Ala Ala
          165          170          175
Asp Asp Cys Glu Phe Leu Arg Ala Glu Leu Asp Glu Leu Arg Gln Arg
          180          185          190
Glu Asp Thr Glu Lys Ala Gln Arg Ser Leu Ser Glu Ile Glu Arg Lys
          195          200          205
Ala Gln Ala Asn Glu Gln Arg Tyr Ser Lys Leu Lys Glu Lys Tyr Ser
210          215          220
Glu Leu Val Gln Asn His Ala Asp Leu Leu Arg Lys Asn Ala Glu Val
225          230          235          240
Thr Lys Gln Val Ser Met Ala Arg Gln Ala Gln Val Asp Leu Glu Arg
          245          250          255
Glu Lys Lys Glu Leu Glu Asp Ser Leu Glu Arg Ile Ser Asp Gln Gly
260          265          270
Gln Arg Lys Thr Gln Glu Gln Leu Glu Val Leu Glu Ser Leu Lys Gln
275          280          285
Glu Leu Gly Thr Ser Gln Arg Glu Leu Gln Val Leu Gln Gly Ser Leu
290          295          300
Glu Thr Ser Ala Gln Ser Glu Ala Asn Trp Ala Ala Glu Phe Ala Glu
305          310          315          320
Leu Glu Lys Glu Arg Asp Ser Leu Val Ser Gly Ala Ala His Arg Glu
          325          330          335
Glu Glu Leu Ser Ala Leu Arg Lys Glu Leu Gln Asp Thr Gln Leu Lys
          340          345          350
Leu Ala Ser Thr Glu Glu Ser Met Cys Gln Leu Ala Lys Asp Gln Arg
          355          360          365
Lys Met Leu Leu Val Gly Ser Arg Lys Ala Ala Glu Gln Val Ile Gln
370          375          380
Asp Ala
385

```

<210> 3
 <211> 4796
 <212> DNA
 <213> Human

<220>
 <221> misc_feature
 <222> (1)...(4796)
 <223> n = A,T,C or G

<400> 3
 cagtgtacgg ttgatcatat aacgccgcgg gcgggggattg gtttatatat cgcaaatgga 60
 tntagggggg gggggatggn cagagatttc gcttcattag gccattataa gcaggaaggg 120
 tttcaaggaa aaaaacccag aaagtgcata ttgcaaccac catgagaaag gggcaacaga 180
 ccttntgttn tgtnttcaac cgctgtcttc tgttttagca acgcagtgtt ttggtggaag 240
 ttgtgccatg tgttccacaa antcttccga gatggacacc cgaacgtcct gaaggacttt 300
 gtgagataca gaaatgaatt gagtgacatg agcaggatgt gggggccacct gagcgagggg 360
 tatggccagc tgtgcagcat ctacctgaaa ctgctaagaa ccaagatgga gtaccacacc 420
 aaaaatccca ggttcccagg caacctgcag atgagtgaac gccagctgga cgaggctgga 480
 gaaagtgcag tgaacaactt tttccagtta acagtggaga tgtttgacta cctggagtgt 540
 gaactcaacc ctcttcaaac agtattcaac tccctggaca tgtcccgtc tgtgtccgtg 600
 acggcagcag ggcagtgcgg cctcgcctcg ctgatccagg tcatcttgga ctgcagccac 660
 ctttatgact acactgtcaa gcttctcttc aaactccact cctgcctccc agctgacacc 720
 ctgcaaggcc accgggaccg cttcatggag cagtttacaa agttgaaaga tctgttctac 780
 cgctccagca acctgcagta cttcaagcgg ctcatccaga tccccagct gcctgagaac 840
 ccacccaact tcctgcgagc ctacgacctg tcagaacata tcagccctgt ggtggtgatc 900
 cctgcagagc cctcatcccc cgacagcgag ccagtcctag agaaggatga cctcatggac 960
 atggatgcct ctacagcaga tttatttgac aacaagtttg atgacatctt tggcagttca 1020
 ttcagcagtg atcccttcaa tttcaacagt caaaatggtg tgaacaagga tgagaaggac 1080
 cacttaattg agcgactata cagagagatc agtggattga aggcacagct agaaaacatg 1140
 aagactgaga gccagcgggt tgtgctgcag ctgaagggcc acgtcagcga gctggaagca 1200
 gatctggccg agcagcagca cctgcggcag caggcggccg acgactgtga attcctgcgg 1260
 gcagaactgg acgagctcag gaggcagcgg gaggacaccg agaaggctca gcggagcctg 1320
 tctgagatga aaaggaaagc tcaagccaat gaacagcgat atagcaagct aaaggagaag 1380
 tacagcgagc tgggtcagaa ccacgctgac ctgctgcgga agaattgcaga ggtgaccaa 1440
 caggtgtcca tggccagaca agcccaggta gatattggaac gagagaaaaa agagctggag 1500
 gattcggttg agcgcatcag tgaccagggc cagcggaaga ctcaagaaca gctggaagtt 1560
 ctgagagagt tgaagcagga acttggcaca agccaacggg agcttcaggt tctgcaaggc 1620
 agcctggaaa cttctgcccc gtcagaagca aactgggcag ccgagttcgc cgagctagag 1680
 aaggagcggg acagcctggt gagtggcgca gctcataggg aggaggaatt atctgctctt 1740
 cggaaagaac tgcaggacac tcagctcaaa ctggccagca cagaggaatc tatgtgccag 1800
 cttgccaaag accaagcga aatgcttctg gttgggtcca ggaaggctgc ggagcaggtg 1860
 atacaagacg ccctgaacca gcttgaagaa cctcctctca tcagctgcgc tgggtctgca 1920
 gatcacctcc tctccacggt cacatccatt tccagctgca tcgagcaact ggagaaaagc 1980
 tggagccagt atctggcctg cccagaagac atcagtgagc ttctccattc cataaccctg 2040
 ctggcccact tgaccagcga cgccattgct catgggtgcca ccacctgcct cagagcccca 2100
 cctgagcctg ccgactcact gaccgaggcc tgtaagcagt atggcaggga aaccctcgcc 2160
 tacctggcct ccctggagga agagggaagc cttgagaatg ccgacagcac agccatgagg 2220
 aactgcctga gcaagatcaa ggccatcggc gaggagctcc tgcccagggg actggacatc 2280
 aagcaggagg agctggggga cctgggtggac aaggagatgg cggccacttc agctgctatt 2340
 gaaacttgca cggccagaat agaggagatg ctacagcaaat cccgagcagg agacacagga 2400
 gtcaaatggg aggtgaatga aaggatcctt cgttgctgta ccagcctcat gcaagctatt 2460
 caggtgctca tcgtggcctc taaggacctc cagagagaga ttgtggagag cggcaggggt 2520
 acagcatccc cttaaagagtt ttatgccaag aactctcgat ggacagaagg acttatctca 2580
 gctccaagg ctgtgggctg gggagccact gtcattggtg atgcagctga tctggtggtg 2640
 caaggcagag ggaaatttga ggagctaatt gttgtttctc atgaaattgc tgctagaca 2700
 gccagccttg tggctgcata caaggtgaaa ctgtgataagg acagcccca cctagcccag 2760
 ctgcagcagg cctctcgggg agtgaaccag gccactgccg gcgttggtgg ctcaaccatt 2820
 tccggcaaat cacagatcga agagacagac aacatggact tctcaagcat gacgctgaca 2880
 cagatcaaac gccaaagat ggattctcag gttaggtgct tagagctaga aatgaattg 2940
 cagaaggagc gtcaaaaact gggagagctt cggaaaaagc actacgagct tgtgtgtgtt 3000
 gctgaggggt ggggaagaag aacagaggca tatccacct cactgcaaga agtggttaacc 3060
 gaaaaagaat agagccaaac caacaccca tctgtcagtg taaatccttg ttacctatct 3120
 cgtgtgtgtt atttccccag ccacaggcca aatccttggg gtcccagggg cagccacacc 3180
 actgccatta cccagtgccg aggcacatgca tgacacttcc caaagatccc tccatagcga 3240
 caccctttct gtttggacc atggtcatct ctgttctttt cccgcctccc tagtttagcat 3300

```

ccaggctggc cagtgtctgc catgagcaag cctaggtacg aagaggggtg gtggggggca 3360
gggccactca acagagagga ccaacatcca gtcctgctga ctatttgacc cccacaacaa 3420
tgggtatcct taatagagga gctgtctgtt gtttgttgac agcttggaag ggaagatct 3480
tatgcctttt cttttctgtt ttcttctcag tcttttcagt ttcattcatt gcacaaactt 3540
gtgagcatca gagggtgat ggattccaaa ccaggacact accctgagat ctgcacagtc 3600
agaaggacgg caggagtgtc ctggctgtga atgccaaagc cattctcccc ctctttgggc 3660
agtgcctagg atttccactg cttcttatgg tggttggttg ggtttttttg ttttgtttt 3720
tttttttaag tttcactcac atagccaact ctcccaaagg gcacaccctt ggggtgagt 3780
ctccagggcc ccccaactgt ggtagctcca gcatggtgc tgcccaggcc tctcgtgct 3840
ccatctccgc ctccacactg accaagtgtt ggcccaccca gtccatgctc cagggtcagg 3900
cggagctgct gagtgcacgc tttcctcaa aagcagaagg agagtgagt cctttccctc 3960
ctaaagctga atcccgccg aaagcctctg tccgccttta caaggagaa gacaacagaa 4020
agagggacaa gagggttcac acagcccagt tcccgtgacg aggtcaaaaa acttgatcac 4080
atgcttgaat ggagctggtg agatcaacaa cactacttcc ctgccgaat gaactgtccg 4140
tgaatggctc ctgtcaagcg ggccgtctcc ctgggccag agacggagt tgggagtgt 4200
tcccaactcc tttctgcaga cgtctgcctt ggcattctct tgaataggaa gatcgttcca 4260
ctttctacgc aattgacaaa cccggaagat catagtcaat tgctcccatc agggaagaac 4320
cctatacttg gtttctacc cttagtattt attactaacc tcccttaagc agcaacagcc 4380
tacaagaga tgcttgagc aatcagaact tcagggtgta ctctagcaaa gctcatcttt 4440
ctgcccggct acatcagcct tcaagaatca gaagaaagcc aaggtgctgg actgttactg 4500
acttggatcc caaagcaagg agatcatttg gagctcttgg gtcagagaaa atgagaaagg 4560
acagagccag cggctccaac tcctttcagc cacatgcccc aggcctctgc tgccctgtgg 4620
acaggatgag gacagagggc acatgaacag cttgccaggg atgggcagcc caacagcact 4680
tttctctctc tagatggacc ccagcattta agtgaccttc tgatcttggg aaaacagcgt 4740
cttctctctt tatctatagc aactcatttg tggtagccat caagcacttc ggaatt 4796

```

<210> 4
 <211> 914
 <212> PRT
 <213> Human

```

<400> 4
Met Ser Arg Met Trp Gly His Leu Ser Glu Gly Tyr Gly Gln Leu Cys
1      5      10      15
Ser Ile Tyr Leu Lys Leu Leu Arg Thr Lys Met Glu Tyr His Thr Lys
20     25     30
Asn Pro Arg Phe Pro Gly Asn Leu Gln Met Ser Asp Arg Gln Leu Asp
35     40     45
Glu Ala Gly Glu Ser Asp Val Asn Phe Phe Gln Leu Thr Val Glu
50     55     60
Met Phe Asp Tyr Leu Glu Cys Glu Leu Asn Leu Phe Gln Thr Val Phe
65     70     75     80
Asn Ser Leu Asp Met Ser Arg Ser Val Ser Val Thr Ala Ala Gly Gln
85     90     95
Cys Arg Leu Ala Pro Leu Ile Gln Val Ile Leu Asp Cys Ser His Leu
100    105    110
Tyr Asp Tyr Thr Val Lys Leu Leu Phe Lys Leu His Ser Cys Leu Pro
115    120    125
Ala Asp Thr Leu Gln Gly His Arg Asp Arg Phe Met Glu Gln Phe Thr
130    135    140
Lys Leu Lys Asp Leu Phe Tyr Arg Ser Ser Asn Leu Gln Tyr Phe Lys
145    150    155    160
Arg Leu Ile Gln Ile Pro Gln Leu Pro Glu Asn Pro Pro Asn Phe Leu
165    170    175
Arg Ala Ser Ala Leu Ser Glu His Ile Ser Pro Val Val Val Ile Pro
180    185    190
Ala Glu Ala Ser Ser Pro Asp Ser Glu Pro Val Leu Glu Lys Asp Asp
195    200    205
Leu Met Asp Met Asp Ala Ser Gln Gln Asn Leu Phe Asp Asn Lys Phe
210    215    220
Asp Asp Ile Phe Gly Ser Ser Phe Ser Ser Asp Pro Phe Asn Phe Asn
225    230    235    240

```

Ser	Gln	Asn	Gly	Val	Asn	Lys	Asp	Glu	Lys	Asp	His	Leu	Ile	Glu	Arg
				245					250					255	
Leu	Tyr	Arg	Glu	Ile	Ser	Gly	Leu	Lys	Ala	Gln	Leu	Glu	Asn	Met	Lys
			260					265					270		
Thr	Glu	Ser	Gln	Arg	Val	Val	Leu	Gln	Leu	Lys	Gly	His	Val	Ser	Glu
			275					280					285		
Leu	Glu	Ala	Asp	Leu	Ala	Glu	Gln	Gln	His	Leu	Arg	Gln	Gln	Ala	Ala
			290				295					300			
Asp	Asp	Cys	Glu	Phe	Leu	Arg	Ala	Glu	Leu	Asp	Glu	Leu	Arg	Arg	Gln
305					310					315					320
Arg	Glu	Asp	Thr	Glu	Lys	Ala	Gln	Arg	Ser	Leu	Ser	Glu	Ile	Glu	Arg
				325					330					335	
Lys	Ala	Gln	Ala	Asn	Glu	Gln	Arg	Tyr	Ser	Lys	Leu	Lys	Glu	Lys	Tyr
			340					345					350		
Ser	Glu	Leu	Val	Gln	Asn	His	Ala	Asp	Leu	Leu	Arg	Lys	Asn	Ala	Glu
		355					360					365			
Val	Thr	Lys	Gln	Val	Ser	Met	Ala	Arg	Gln	Ala	Gln	Val	Asp	Leu	Glu
	370					375					380				
Arg	Glu	Lys	Lys	Glu	Leu	Glu	Asp	Ser	Leu	Glu	Arg	Ile	Ser	Asp	Gln
385					390					395					400
Gly	Gln	Arg	Lys	Thr	Gln	Glu	Gln	Leu	Glu	Val	Leu	Glu	Ser	Leu	Lys
				405					410					415	
Gln	Glu	Leu	Gly	Thr	Ser	Gln	Arg	Glu	Leu	Gln	Val	Leu	Gln	Gly	Ser
			420					425					430		
Leu	Glu	Thr	Ser	Ala	Gln	Ser	Glu	Ala	Asn	Trp	Ala	Ala	Glu	Phe	Ala
		435					440					445			
Glu	Leu	Glu	Lys	Glu	Arg	Asp	Ser	Leu	Val	Ser	Gly	Ala	Ala	His	Arg
	450					455					460				
Glu	Glu	Glu	Leu	Ser	Ala	Leu	Arg	Lys	Glu	Leu	Gln	Asp	Thr	Gln	Leu
465					470					475					480
Lys	Leu	Ala	Ser	Thr	Glu	Glu	Ser	Met	Cys	Gln	Leu	Ala	Lys	Asp	Gln
				485					490					495	
Arg	Lys	Met	Leu	Val	Gly	Ser	Arg	Lys	Ala	Ala	Glu	Gln	Val	Ile	
		500					505					510			
Gln	Asp	Ala	Leu	Asn	Gln	Leu	Glu	Glu	Pro	Pro	Leu	Ile	Ser	Cys	Ala
		515					520					525			
Gly	Ser	Ala	Asp	His	Leu	Leu	Ser	Thr	Val	Thr	Ser	Ile	Ser	Ser	Cys
	530					535					540				
Ile	Glu	Gln	Leu	Glu	Lys	Ser	Trp	Ser	Gln	Tyr	Leu	Ala	Cys	Pro	Glu
545					550					555					560
Asp	Ile	Ser	Gly	Leu	Leu	His	Ser	Ile	Thr	Leu	Leu	Ala	His	Leu	Thr
				565					570					575	
Ser	Asp	Ala	Ile	Ala	His	Gly	Ala	Thr	Thr	Cys	Leu	Arg	Ala	Pro	Pro
		580						585					590		
Glu	Pro	Ala	Asp	Ser	Leu	Thr	Glu	Ala	Cys	Lys	Gln	Tyr	Gly	Arg	Glu
		595					600					605			
Thr	Leu	Ala	Tyr	Leu	Ala	Ser	Leu	Glu	Glu	Glu	Gly	Ser	Leu	Glu	Asn
	610					615					620				
Ala	Asp	Ser	Thr	Ala	Met	Arg	Asn	Cys	Leu	Ser	Lys	Ile	Lys	Ala	Ile
625					630					635					640
Gly	Glu	Glu	Leu	Leu	Pro	Arg	Gly	Leu	Asp	Ile	Lys	Gln	Glu	Glu	Leu
				645					650					655	
Gly	Asp	Leu	Val	Asp	Lys	Glu	Met	Ala	Ala	Thr	Ser	Ala	Ala	Ile	Glu
			660					665					670		
Thr	Cys	Thr	Ala	Arg	Ile	Glu	Glu	Met	Leu	Ser	Lys	Ser	Arg	Ala	Gly
		675					680					685			
Asp	Thr	Gly	Val	Lys	Leu	Glu	Val	Asn	Glu	Arg	Ile	Leu	Arg	Cys	Cys
	690					695					700				
Thr	Ser	Leu	Met	Gln	Ala	Ile	Gln	Val	Leu	Ile	Val	Ala	Ser	Lys	Asp
705					710					715					720
Leu	Gln	Arg	Glu	Ile	Val	Glu	Ser	Gly	Arg	Gly	Thr	Ala	Ser	Pro	Lys
				725					730					735	

Glu Phe Tyr Ala Lys Asn Ser Arg Trp Thr Glu Gly Leu Ile Ser Ala
 740 745 750
 Ser Lys Ala Val Gly Trp Gly Ala Thr Val Met Val Asp Ala Ala Asp
 755 760 765
 Leu Val Val Gln Gly Arg Gly Lys Phe Glu Glu Leu Met Val Cys Ser
 770 775 780
 His Glu Ile Ala Ala Ser Thr Ala Gln Leu Val Ala Ala Ser Lys Val
 785 790 795 800
 Lys Ala Asp Lys Asp Ser Pro Asn Leu Ala Gln Leu Gln Gln Ala Ser
 805 810 815
 Arg Gly Val Asn Gln Ala Thr Ala Gly Val Val Ala Ser Thr Ile Ser
 820 825 830
 Gly Lys Ser Gln Ile Glu Glu Thr Asp Asn Met Asp Phe Ser Ser Met
 835 840 845
 Thr Leu Thr Gln Ile Lys Arg Gln Glu Met Asp Ser Gln Val Arg Val
 850 855 860
 Leu Glu Leu Glu Asn Glu Leu Gln Lys Glu Arg Gln Lys Leu Gly Glu
 865 870 875 880
 Leu Arg Lys Lys His Tyr Glu Leu Ala Gly Val Ala Glu Gly Trp Glu
 885 890 895
 Glu Gly Thr Glu Ala Ser Pro Pro Thr Leu Gln Glu Val Val Thr Glu
 900 905 910
 Lys Glu

<210> 5
 <211> 1090
 <212> PRT
 <213> Human

<400> 5
 Met Leu Leu Cys Gln Gly Ser Glu Trp Arg Arg Asp Gln Gln Leu Gly
 1 5 10 15
 Thr Ala Asn Ala Arg Gln Trp Cys Pro Leu Pro Gln Asp Ala Gln Pro
 20 25 30
 Ala Gly Ser Trp Glu Arg Cys Pro Pro Leu Pro Pro Ala Gly Arg Leu
 35 40 45
 Gln Gly Thr Asp His Pro Trp Gly Trp Gly Arg Leu Ala Gly Gly Gly
 50 55 60
 Glu Arg Gly Gly Leu Trp Glu Gly Leu Ser His Ser Gln Arg Leu Ile
 65 70 75 80
 His Leu Ile Leu Leu Ser Leu Pro Leu Leu Val Phe Gln Thr Val Ser
 85 90 95
 Ile Asn Lys Ala Ile Asn Thr Gln Glu Val Ala Val Lys Glu Lys His
 100 105 110
 Ala Arg Thr Cys Ile Leu Gly Thr His His Glu Lys Gly Ala Gln Thr
 115 120 125
 Phe Trp Ser Val Val Asn Arg Leu Pro Leu Ser Ser Asn Ala Val Leu
 130 135 140
 Cys Trp Lys Phe Cys His Val Phe His Lys Leu Leu Arg Asp Gly His
 145 150 155 160
 Pro Asn Val Leu Lys Asp Ser Leu Arg Tyr Arg Asn Glu Leu Ser Asp
 165 170 175
 Met Ser Arg Met Trp Gly His Leu Ser Glu Gly Tyr Gly Gln Leu Cys
 180 185 190
 Ser Ile Tyr Leu Lys Leu Leu Arg Thr Lys Met Glu Tyr His Thr Lys
 195 200 205
 Asn Pro Arg Phe Pro Gly Asn Leu Gln Met Ser Asp Arg Gln Leu Asp
 210 215 220
 Glu Ala Gly Glu Ser Asp Val Asn Asn Phe Phe Gln Leu Thr Val Glu
 225 230 235 240
 Met Phe Asp Tyr Leu Glu Cys Glu Leu Asn Leu Phe Gln Thr Val Phe

Asn	Ser	Leu	Asp	Met	Ser	Arg	Ser	Val	Ser	Val	Thr	Ala	Ala	Gly	Gln
			260					265						270	
Cys	Arg	Leu	Ala	Pro	Leu	Ile	Gln	Val	Ile	Leu	Asp	Cys	Ser	His	Leu
		275					280					285			
Tyr	Asp	Tyr	Thr	Val	Lys	Leu	Phe	Lys	Leu	His	Ser	Cys	Leu	Pro	
	290				295					300					
Ala	Asp	Thr	Leu	Gln	Gly	His	Arg	Asp	Arg	Phe	Met	Glu	Gln	Phe	Thr
305					310					315				320	
Lys	Leu	Lys	Asp	Leu	Phe	Tyr	Arg	Ser	Ser	Asn	Leu	Gln	Tyr	Phe	Lys
			325					330						335	
Arg	Leu	Ile	Gln	Ile	Pro	Gln	Leu	Pro	Glu	Asn	Pro	Pro	Asn	Phe	Leu
		340						345					350		
Arg	Ala	Ser	Ala	Leu	Ser	Glu	His	Ile	Ser	Pro	Val	Val	Val	Ile	Pro
	355					360						365			
Ala	Glu	Ala	Ser	Ser	Pro	Asp	Ser	Glu	Pro	Val	Leu	Glu	Lys	Asp	Asp
	370				375						380				
Leu	Met	Asp	Met	Asp	Ala	Ser	Gln	Gln	Asn	Leu	Phe	Asp	Asn	Lys	Phe
385					390					395				400	
Asp	Asp	Ile	Phe	Gly	Ser	Ser	Phe	Ser	Ser	Asp	Pro	Phe	Asn	Phe	Asn
			405					410						415	
Ser	Gln	Asn	Gly	Val	Asn	Lys	Asp	Glu	Lys	Asp	His	Leu	Ile	Glu	Arg
		420						425					430		
Leu	Tyr	Arg	Glu	Ile	Ser	Gly	Leu	Lys	Ala	Gln	Leu	Glu	Asn	Met	Lys
	435					440						445			
Thr	Glu	Ser	Gln	Arg	Val	Val	Leu	Gln	Leu	Lys	Gly	His	Val	Ser	Glu
	450					455					460				
Leu	Glu	Ala	Asp	Leu	Ala	Glu	Gln	Gln	His	Leu	Arg	Gln	Gln	Ala	Ala
465					470					475				480	
Asp	Asp	Cys	Glu	Phe	Leu	Arg	Ala	Glu	Leu	Asp	Glu	Leu	Arg	Arg	Gln
			485					490						495	
Arg	Glu	Asp	Thr	Glu	Lys	Ala	Gln	Arg	Ser	Leu	Ser	Glu	Ile	Glu	Arg
		500						505					510		
Lys	Ala	Gln	Ala	Asn	Glu	Gln	Arg	Tyr	Ser	Lys	Leu	Lys	Glu	Lys	Tyr
		515					520					525			
Ser	Glu	Leu	Val	Gln	Asn	His	Ala	Asp	Leu	Leu	Arg	Lys	Asn	Ala	Glu
	530				535						540				
Val	Thr	Lys	Gln	Val	Ser	Met	Ala	Arg	Gln	Ala	Gln	Val	Asp	Leu	Glu
545					550					555				560	
Arg	Glu	Lys	Lys	Glu	Leu	Glu	Asp	Ser	Leu	Glu	Arg	Ile	Ser	Asp	Gln
			565					570						575	
Gly	Gln	Arg	Lys	Thr	Gln	Glu	Gln	Leu	Glu	Val	Leu	Glu	Ser	Leu	Lys
		580						585					590		
Gln	Glu	Leu	Ala	Thr	Ser	Gln	Arg	Glu	Leu	Gln	Val	Leu	Gln	Gly	Ser
	595					600						605			
Leu	Glu	Thr	Ser	Ala	Gln	Ser	Glu	Ala	Asn	Trp	Ala	Ala	Glu	Phe	Ala
	610					615					620				
Glu	Leu	Glu	Lys	Glu	Arg	Asp	Ser	Leu	Val	Ser	Gly	Ala	Ala	His	Arg
625					630					635				640	
Glu	Glu	Glu	Leu	Ser	Ala	Leu	Arg	Lys	Glu	Leu	Gln	Asp	Thr	Gln	Leu
			645						650					655	
Lys	Leu	Ala	Ser	Thr	Glu	Glu	Ser	Met	Cys	Gln	Leu	Ala	Lys	Asp	Gln
		660						665					670		
Arg	Lys	Met	Leu	Leu	Val	Gly	Ser	Arg	Lys	Ala	Ala	Glu	Gln	Val	Ile
	675					680						685			
Gln	Asp	Ala	Leu	Asn	Gln	Leu	Glu	Glu	Pro	Pro	Leu	Ile	Ser	Cys	Ala
	690					695					700				
Gly	Ser	Ala	Asp	His	Leu	Leu	Ser	Thr	Val	Thr	Ser	Ile	Ser	Ser	Cys
705					710					715				720	
Ile	Glu	Gln	Leu	Glu	Lys	Ser	Trp	Ser	Gln	Tyr	Leu	Ala	Cys	Pro	Glu
			725					730					735		
Asp	Ile	Ser	Gly	Leu	Leu	His	Ser	Ile	Thr	Leu	Leu	Ala	His	Leu	Thr

<210> 6
<211> 3251
<212> DNA
<213> Human

- 8 -


```

ccaggagcag ggcgagttgc agggccggct ggcagagagg gagtctcagg agcaggggct 660
gccccagagg ctgctggacg agcagttcgc agtgttgccg ggcgctgctg ccgaggccgc 720
gggcatcctg caggatgccg tgagcaagct ggacgacccc ctgcacctgc gctgtaccag 780
ctccccagac tacctggtga gcagggccca ggaggccttg gatgccgtga gcacctgga 840
ggagggccac gccacgtacc tgacctcctt ggcagacgcc tccgcccctg tggcagctct 900
gacccgcttc tcccacctgg ctgcggtatc catcatcaat ggcggtgcc a cctcgacct 960
ggctcccacc gacctgccc accgcctcat agacacctgc agggagtgcg gggcccgggc 1020
tctggagctc atggggcagc tgcaggacca gcaggctctg cggcacatgc agggcagcct 1080
ggtgcccaga cccctgcagg gcatccttca gctgggcca a gaactgaaac ccaagagcct 1140
agatgtgcgg caggaggagc tggggggcgt ggtcgacaag gagatggcgg ccacatccgc 1200
agccattgaa gatgctgtgc ggaggattga ggacatgatg aaccaggcac gccacgccag 1260
ctcgggggtg aagctggagg tgaacgagag gatcctcaac tcctgcacag acctgatgaa 1320
ggctatccgg ctctgtgtga cgacatccac tagcctgcag aaggagatcg tggagagcgg 1380
caggggggca gccacgcagc aggaatttta cgccaagaac tcgcgctgga ccgaaggcct 1440
catctcggcc tccaaggctg tgggctgggg agccacacag ctggtggagg cagctgacaa 1500
ggtggtgctt cacacgggca agtatgagga gctcatcgtc tgctcccacg agatcgagc 1560
cagcacggcc cagctggtgg cggcctccaa ggtgaaggcc aacaagcaca gccccacct 1620
gagccgcctg caggaatggt ctgcacagt caatgagagg gctgccaatg tggttggcctc 1680
caccaagtca ggccaggagc agattgagga cagagacacc atggatttct ccggcctgtc 1740
cctcatcaag ctgaagaagc aggagatgga gacgcagggt cgtgtcctgg agctggagaa 1800
gacgctggag gctgaacgca tgcggctggg ggagttgcgg aagcaacact acgtgctggc 1860
tggggcatca ggcagccctg gagaggaggt ggccatccgg ccagcactg cccccgaag 1920
tgtaaccacc aagaaccac ccctggccca gaagcccagc gtggccccc a gacaggacca 1980
ccagcttgac aaaaaggatg gcatctacc agctcaactc gtgaactact agggccccc 2040
gggttccagc aggggtggctg gtgacaggcc tgggcctctg caactgccct gacaggaccg 2100
agaggccttg cccctccacc tgggtgccaa gcctcccgc ccaccgtctg gatcaatgtc 2160
ctcaaggccc ctggccctta ctgagcctgc agggctcctg gccatgtggg tgggtcttct 2220
ggatgtgagt ctcttattta tctgcagaag gaactttggg gtgcagccag gaccggtag 2280
gcctgagcct caactcttca gaaaatagt tttttaatat tctcttctag aaaaatagt 2340
ttttaatatt ccgagctaga gctcttctt ctacgtttgt agtcagcaca ctgggaaacc 2400
ggggcaggct ggggctccct gccttctgga ctctggaagg tctgtgatgg atggaaggca 2460
cacagccggt gccggctgat gggacgaggg tcaggcatcc tgtctgtggc cttctggggc 2520
accgattcta ccaggccctc cagctgcgtg gtctccgcag accaggctct gtgtgggcta 2580
gaggaatgtc gccattacc tctcagggcc ctggccctcg ggcctccgtg atgggagccc 2640
cccaggagg gtcagatgct ggaaggggcc gcttctggg gagtgaggtg agacatagcg 2700
gccaggcgc tgccttcaact cctggagttt ccatttccag ctggaatctg cagccacccc 2760
catttctctg tttccattcc cccgttcttg ccgcgccc a ctgcccacct gaaggggtg 2820
tttccagccc tccggagagt gggcttggcc ctaggccctc cagctcagcc agaaaaagcc 2880
cagaaaccca ggtgctggac cagggccctc agggaggag cctgcccgtg gagtgggcta 2940
ggccctggct ttgcccgtca gatttgaacg aatgtgtgtc ccttgagccc aaggagagcg 3000
gcaggagggg tgggaccagg ctgggaggac agagccagca gctgccatgc cctcctgtc 3060
ccccacccc agccctagcc cttagcctt tcaccctgtg ctctggaaag gctaccaa 3120
actggccaag gtcaggagga gcaaaaatga gccagcacca gcgccttggc tttgtgttag 3180
catttctctc tgaagtgttc tgttggaat aaaatgcact ttgactgtta aaaaaaaaa 3240
aaaaaaaaa a 3251

```

<210> 7
 <211> 676
 <212> PRT
 <213> Human

<400> 7
 Gly Glu Leu Glu Glu Gln Arg Lys Gln Lys Gln Lys Ala Leu Val Asp
 1 5 10 15
 Asn Glu Gln Leu Arg His Glu Leu Ala Gln Leu Arg Ala Ala Gln Leu
 20 25 30
 Glu Arg Glu Arg Ser Gln Gly Leu Arg Glu Glu Ala Glu Arg Lys Ala
 35 40 45
 Ser Ala Thr Glu Ala Arg Tyr Asn Lys Leu Lys Glu Lys His Ser Glu
 50 55 60
 Leu Val His Val His Ala Glu Leu Leu Arg Lys Asn Ala Asp Thr Ala
 65 70 75 80

Lys Gln Leu Thr Val Thr Gln Gln Ser Gln Glu Glu Val Ala Arg Val
 85 90 95
 Lys Glu Gln Leu Ala Phe Gln Val Glu Gln Val Lys Arg Glu Ser Glu
 100 105 110
 Leu Lys Leu Glu Glu Lys Ser Asp Gln Gln Glu Lys Leu Lys Arg Glu
 115 120 125
 Leu Glu Ala Lys Ala Gly Glu Leu Ala Arg Ala Gln Glu Ala Leu Ser
 130 135 140
 His Thr Glu Gln Ser Lys Ser Glu Leu Ser Ser Arg Leu Asp Thr Leu
 145 150 155 160
 Ser Ala Glu Lys Asp Ala Leu Ser Gly Ala Val Arg Gln Arg Glu Ala
 165 170 175
 Asp Leu Leu Ala Ala Gln Ser Leu Val Arg Glu Thr Glu Ala Ala Leu
 180 185 190
 Ser Arg Glu Gln Gln Arg Ser Ser Gln Glu Gln Gly Glu Leu Gln Gly
 195 200 205
 Arg Leu Ala Glu Arg Glu Ser Gln Glu Gln Gly Leu Arg Gln Arg Leu
 210 215 220
 Leu Asp Glu Gln Phe Ala Val Leu Arg Gly Ala Ala Ala Glu Ala Ala
 225 230 235 240
 Gly Ile Leu Gln Asp Ala Val Ser Lys Leu Asp Asp Pro Leu His Leu
 245 250 255
 Arg Cys Thr Ser Ser Pro Asp Tyr Leu Val Ser Arg Ala Gln Glu Ala
 260 265 270
 Leu Asp Ala Val Ser Thr Leu Glu Gly His Ala Gln Tyr Leu Thr
 275 280 285
 Ser Leu Ala Asp Ala Ser Ala Leu Val Ala Ala Leu Thr Arg Phe Ser
 290 295 300
 His Leu Ala Ala Asp Thr Ile Ile Asn Gly Gly Ala Thr Ser His Leu
 305 310 315 320
 Ala Pro Thr Asp Pro Ala Asp Arg Leu Ile Asp Thr Cys Arg Glu Cys
 325 330 335
 Gly Ala Arg Ala Leu Glu Leu Met Gly Gln Leu Gln Asp Gln Gln Ala
 340 345 350
 Leu Arg His Met Gln Ala Ser Leu Val Arg Thr Pro Leu Gln Gly Ile
 355 360 365
 Leu Gln Leu Gly Gln Glu Leu Lys Pro Lys Ser Leu Asp Val Arg Gln
 370 375 380
 Glu Glu Leu Gly Ala Val Val Asp Lys Glu Met Ala Ala Thr Ser Ala
 385 390 395 400
 Ala Ile Glu Asp Ala Val Arg Arg Ile Glu Asp Met Met Asn Gln Ala
 405 410 415
 Arg His Ala Ser Ser Gly Val Lys Leu Glu Val Asn Glu Arg Ile Leu
 420 425 430
 Asn Ser Cys Thr Asp Leu Met Lys Ala Ile Arg Leu Leu Val Thr Thr
 435 440 445
 Ser Thr Ser Leu Gln Lys Glu Ile Val Glu Ser Gly Arg Gly Ala Ala
 450 455 460
 Thr Gln Gln Glu Phe Tyr Ala Lys Asn Ser Arg Trp Thr Glu Gly Leu
 465 470 475 480
 Ile Ser Ala Ser Lys Ala Val Gly Trp Gly Ala Thr Gln Leu Val Glu
 485 490 495
 Ala Ala Asp Lys Val Val Leu His Thr Gly Lys Tyr Glu Glu Leu Ile
 500 505 510
 Val Cys Ser His Glu Ile Ala Ala Ser Thr Ala Gln Leu Val Ala Ala
 515 520 525
 Ser Lys Val Lys Ala Asn Lys His Ser Pro His Leu Ser Arg Leu Gln
 530 535 540
 Glu Cys Ser Arg Thr Val Asn Glu Arg Ala Ala Asn Val Val Ala Ser
 545 550 555 560
 Thr Lys Ser Gly Gln Glu Gln Ile Glu Asp Arg Asp Thr Met Asp Phe
 565 570 575

Ser Gly Leu Ser Leu Ile Lys Leu Lys Lys Gln Glu Met Glu Thr Gln
 580 585 590
 Val Arg Val Leu Glu Leu Glu Lys Thr Leu Glu Ala Glu Arg Met Arg
 595 600 605
 Leu Gly Glu Leu Arg Lys Gln His Tyr Val Leu Ala Gly Ala Ser Gly
 610 615 620
 Ser Pro Gly Glu Glu Val Ala Ile Arg Pro Ser Thr Ala Pro Arg Ser
 625 630 635 640
 Val Thr Thr Lys Lys Pro Pro Leu Ala Gln Lys Pro Ser Val Ala Pro
 645 650 655
 Arg Gln Asp His Gln Leu Asp Lys Lys Asp Gly Ile Tyr Pro Ala Gln
 660 665 670
 Leu Val Asn Tyr
 675

<210> 8
 <211> 2301
 <212> DNA
 <213> Mouse

<400> 8
 ggcacgaggg ctcattcaga tccccagct gcccgagaat ccacccaact tcctacgagc 60
 ctcgcccttg tcagagcaca tcagtcctgt ggtggtgatc ccggcagagg tgtcatcccc 120
 agacagtgg cctgtcctgg agaaggatga cctcatggac atggacgcct ccagcagac 180
 tttgtttgac aacaagtttg atgacgtctt tggcagctca ttgagcagcg accctttcaa 240
 tttcaacaat caaaatggcg tgaacaagga cgagaaggac cacttgattg aacgcctgta 300
 cagagagatc agtggactga cagggcagct ggacaacatg aagattgaga gccagcgggc 360
 catgctgcag ctgaagggtc gagtgaagtga gctggaggca gagctagcag agcagcagca 420
 cttgggcccgg caggctatgg atgactgcga gttcctgcgc actgagctgg atgaactgaa 480
 gaggcagcga gaggacacgg agaaggcaca gcgcagcctg actgagatag aaagaaaggc 540
 ccaggctaag gaacagaggt atagcaagtt aaaagagaag tacagtgaac tgggtgcagaa 600
 ccatgctgac ctgctgcgga agaacgcaga ggtgaccaa caggtgtccg tggcccggca 660
 agcccagggtg gatttggaaa gagagaaaaa agagctagca gattcctttg cacgtgtaag 720
 tgaccaggcc cagcggaaga ctcaagagca acaggatggt ctagagaacc tgaagcatga 780
 actggccacc agcagacagg agctgcaggt cctccacagc aacctggaaa cctctgcca 840
 gtcagaagcg aaatggctga cacagatcgc cgagttggag aaggaacaag gcagcttggc 900
 gactgttgca gctcagagag aggaagagtt atcagccctc cgagaccagc tggaaagcac 960
 ccagatcaag ctggctgggg cccaggaatc catgtgccag caggtgaagg accagaggaa 1020
 aaccctcttg gcagggtgc ggaaggctgc ggagcgtgag atacaggagg cgctgagcca 1080
 gcttgaggaa cccaccctca tcagctgtgc aggatccaca gatcaccttc tctccaaagt 1140
 cagctccgtt tccagctgcc tcgagcaact ggaaaagaac ggcagccagt atctggcctg 1200
 ccagaagat attagtgcgc ttctgcactc gatcacctcg cttgcccact tgaccggtga 1260
 cactgtcatc caggggagtg ccaccagcct ccgggcccga ccggagccag ccgactcgtt 1320
 gacggaggcc tgtaggcagt atggcagaga aacctgggcc tatctgtcct ccctggagga 1380
 agaggggaact gtggagaatg ctgacgtcac agcccttagg aattgcctca gcagggtcaa 1440
 gacccttggc gaggagctgc tgcccagggg cctggacatc aagcaggaag agctgggtga 1500
 cctggtggac aaggagatgg cagccacttc agctgccatt gaagctgcca ccaccggat 1560
 agagggaaatt ctcaagtaag cccgagcagg agcacaggga gtcaagctgg aggtgaatga 1620
 gaggatcctg ggttcctgta ccagcctgat gcaggccatc aaggtgctcg ttgtggcctc 1680
 caaggacctc cagaaggaga tagtggagag tggcaggggt agtgcattcc ctaaagaatt 1740
 ttacgccaaag aactctcggt ggacggaagg gctgatattc gcctccaaag ctgttggttg 1800
 gggagctacc atcatggttg atgctgctga tcttgtggtc caaggcaaag ggaagttcga 1860
 ggagctgatg gtgtgttcac gcgagattgc tgccagtact gccagctcg tggctgcac 1920
 caaggtgaaa gcgaacaagg gcagcctcaa tctgaccag ctgcagcagg cctctcgagg 1980
 agtgaaccag gccacagccg ctgtgggtggc ctcaaccatt tctggcaaat ctcaagattga 2040
 ggaaacagac agtatggact tctcaagcat gacatgacc cagatcaagc gccaggagat 2100
 ggattcccag gttaggtgac tggagctgga aaatgacctg cagaaggagc gtcagaaact 2160
 aggagagcta cggaagaaac actacgagct ggaggcgctg gctgagggct gggagggaag 2220
 gacagaagca tcaccgtcta ctgtccaaga agcaataacc gacaaagagt agagccaagc 2280
 cgacacccca cacatcagaa a

<210> 9

<211> 756
 <212> PRT
 <213> Mouse

<400> 9
 Ala Arg Gly Leu Ile Gln Ile Pro Gln Leu Pro Glu Asn Pro Pro Asn
 1 5 10 15
 Phe Leu Arg Ala Ser Ala Leu Ser Glu His Ile Ser Pro Val Val Val
 20 25 30
 Ile Pro Ala Glu Val Ser Ser Pro Asp Ser Glu Pro Val Leu Glu Lys
 35 40 45
 Asp Asp Leu Met Asp Met Asp Ala Ser Gln Gln Thr Leu Phe Asp Asn
 50 55 60
 Lys Phe Asp Asp Val Phe Gly Ser Ser Leu Ser Ser Asp Pro Phe Asn
 65 70 75 80
 Phe Asn Asn Gln Asn Gly Val Asn Lys Asp Glu Lys Asp His Leu Ile
 85 90 95
 Glu Arg Leu Tyr Arg Glu Ile Ser Gly Leu Thr Gly Gln Leu Asp Asn
 100 105 110
 Met Lys Ile Glu Ser Gln Arg Ala Met Leu Gln Leu Lys Gly Arg Val
 115 120 125
 Ser Glu Leu Glu Ala Glu Leu Ala Glu Gln Gln His Leu Gly Arg Gln
 130 135 140
 Ala Met Asp Asp Cys Glu Phe Leu Arg Thr Glu Leu Asp Glu Leu Lys
 145 150 155 160
 Arg Gln Arg Glu Asp Thr Glu Lys Ala Gln Arg Ser Leu Thr Glu Ile
 165 170 175
 Glu Arg Lys Ala Gln Ala Asn Glu Gln Arg Tyr Ser Lys Leu Lys Glu
 180 185 190
 Lys Tyr Ser Glu Leu Val Gln Asn His Ala Asp Leu Leu Arg Lys Asn
 195 200 205
 Ala Glu Val Thr Lys Gln Val Ser Val Ala Arg Gln Ala Gln Val Asp
 210 215 220
 Leu Glu Arg Glu Lys Lys Glu Leu Ala Asp Ser Phe Ala Arg Val Ser
 225 230 235 240
 Asp Gln Ala Gln Arg Lys Thr Gln Glu Gln Gln Asp Val Leu Glu Asn
 245 250 255
 Leu Lys His Glu Leu Ala Thr Ser Arg Gln Glu Leu Gln Val Leu His
 260 265 270
 Ser Asn Leu Glu Thr Ser Ala Gln Ser Glu Ala Lys Trp Leu Thr Gln
 275 280 285
 Ile Ala Glu Leu Glu Lys Glu Gln Gly Ser Leu Ala Thr Val Ala Ala
 290 295 300
 Gln Arg Glu Glu Glu Leu Ser Ala Leu Arg Asp Gln Leu Glu Ser Thr
 305 310 315 320
 Gln Ile Lys Leu Ala Gly Ala Gln Glu Ser Met Cys Gln Gln Val Lys
 325 330 335
 Asp Gln Arg Lys Thr Leu Leu Ala Gly Ile Arg Lys Ala Ala Glu Arg
 340 345 350
 Glu Ile Gln Glu Ala Leu Ser Gln Leu Glu Glu Pro Thr Leu Ile Ser
 355 360 365
 Cys Ala Gly Ser Thr Asp His Leu Leu Ser Lys Val Ser Ser Val Ser
 370 375 380
 Ser Cys Leu Glu Gln Leu Glu Lys Asn Gly Ser Gln Tyr Leu Ala Cys
 385 390 395 400
 Pro Glu Asp Ile Ser Glu Leu Leu His Ser Ile Thr Leu Leu Ala His
 405 410 415
 Leu Thr Gly Asp Thr Val Ile Gln Gly Ser Ala Thr Ser Leu Arg Ala
 420 425 430
 Pro Pro Glu Pro Ala Asp Ser Leu Thr Glu Ala Cys Arg Gln Tyr Gly
 435 440 445
 Arg Glu Thr Leu Ala Tyr Leu Ser Ser Leu Glu Glu Glu Gly Thr Val

450	455	460
Glu Asn Ala Asp Val	Thr Ala Leu Arg Asn Cys	Leu Ser Arg Val Lys
465	470	475
Thr Leu Gly Glu Glu	Leu Leu Pro Arg Gly Leu	Asp Ile Lys Gln Glu
	485	490
Glu Leu Gly Asp Leu	Val Asp Lys Glu Met Ala Ala	Thr Ser Ala Ala
	500	505
Ile Glu Ala Ala Thr	Thr Arg Ile Glu Glu Ile Leu	Ser Lys Ser Arg
	515	520
Ala Gly Asp Thr Gly	Val Lys Leu Glu Val Asn Glu	Arg Ile Leu Gly
	530	535
Ser Cys Thr Ser Leu	Met Gln Ala Ile Lys Val	Leu Val Val Ala Ser
545	550	555
Lys Asp Leu Gln Lys	Glu Ile Val Glu Ser Gly	Arg Gly Ser Ala Ser
	565	570
Pro Lys Glu Phe Tyr	Ala Lys Asn Ser Arg Trp	Thr Glu Gly Leu Ile
	580	585
Ser Ala Ser Lys Ala	Val Gly Trp Gly Ala Thr	Ile Met Val Asp Ala
	595	600
Ala Asp Leu Val Val	Gln Gly Lys Gly Lys Phe	Glu Glu Leu Met Val
	610	615
Cys Ser Arg Glu Ile	Ala Ala Ser Thr Ala	Gln Leu Val Ala Ala Ser
625	630	635
Lys Val Lys Ala Asn	Lys Gly Ser Leu Asn	Leu Thr Gln Leu Gln
	645	650
Ala Ser Arg Gly Val	Asn Gln Ala Thr Ala	Ala Val Val Ala Ser Thr
	660	665
Ile Ser Gly Lys Ser	Gln Ile Glu Glu Thr Asp	Ser Met Asp Phe Ser
	675	680
Ser Met Thr Leu Thr	Gln Ile Lys Arg Gln Glu	Met Asp Ser Gln Val
	690	695
Arg Val Leu Glu Leu	Glu Asn Asp Leu Gln Lys	Glu Arg Gln Lys Leu
705	710	715
Gly Glu Leu Arg Lys	Lys His Tyr Glu Leu Glu	Gly Val Ala Glu Gly
	725	730
Trp Glu Glu Gly Thr	Glu Ala Ser Pro Ser	Thr Val Gln Glu Ala Ile
	740	745
Pro Asp Lys Glu		750
	755	

<210> 10
 <211> 3979
 <212> DNA
 <213> Mouse

<400> 10					
ggcagcaggc	ggcgcgcggc	ctccgtgtgc	ctaggcttga	ggcgggcggt	gacgcctcat
tcgcgcggag	ccgggcccgg	acacggtcgg	cggcagcatg	aacagcatca	agaatgtgcc
ggcgcggtg	ctgagccgca	ggccggggcca	cagcctagag	gccgagcgcg	agcagttcga
caagacgcag	gccatcagta	tcagcaaagc	catcaacagc	caggaggccc	cagtgaagga
gaagcatgcc	cggcgatatca	tcctggggcac	gcacatgag	aaggggagcct	tcaccttctg
gtcctatgcc	atcggcctgc	cgctgtccag	cagctccatc	ctcagctgga	agttctgtca
cgctccttcac	aaggtcctcc	gggacggaca	ccccaacgtc	ctgcatgact	atcagcggta
ccggagcaac	atacgtgaga	tcggtgactt	gtggggccac	cttcgtgacc	agtatggaca
cctggtgaat	atctatacca	aactgttgct	gactaagatc	tccttccacc	ttaagcacc
ccagtttcc	gcaggcctgg	aggtaacaga	tgaggtgttg	gagaaggcgg	cgggaaactga
tgtaacaac	atttttcagc	ttaccgtgga	gatgtttgac	tacatggact	gtgaactgaa
gctttctgag	tcagttttcc	ggcagctcaa	cacggccatc	gcagtgtccc	agatgtcttc
tggccagtgt	cgcttagcgc	cgctcatcca	ggtcattcag	gactgcagcc	acctgtacca
ctacacagt	aagctcatgt	ttaagctgca	gtcctgtctc	ccggcagaca	ccctgcaagg
ccacagggat	cggttccacg	agcagttcca	cagcctcaaa	aacttcttcc	gccgggcttc
agacatgctg	tacttcaaga	ggctcatcca	gatccccg	ctgcctgagg	gaccccccaa
					60
					120
					180
					240
					300
					360
					420
					480
					540
					600
					660
					720
					780
					840
					900
					960

```

tttccctgcgg gcttcagccc tggctgagca catcaagccg gtgggtggtga ttccccgagga 1020
ggccccagag gaagaggagc ctgagaacct aattgaaatc agcagtgcgc cccctgctgg 1080
ggagccagtg gtgggtggctg acctctttga tcagaccttt ggacccccca atggctccat 1140
gaaggatgac agggacctcc aaatcgagaa cttgaagaga gaggtggaga ccctccgtgc 1200
tgagctggag aagattaaga tggaggcaca gcggtacatc tcccagctga agggccaggt 1260
gaatggcctg gaggcagagc tggaggagca gcgcaagcag aagcagaagg ccctggtgga 1320
caacgagcag ctgcgccacg agctggccca gctcaaggcc ctgcagctgg agggcgccccg 1380
caaccagggc cttcgagagg aagcagagag gaaggccagt gccacggagg cacgctacag 1440
caagctgaag gagaaacaca gcgaactcat taacacgcac gccgagctgc tcaggaagaa 1500
cgcagacacg gccaagcagc tgacagtgc acagcagagc caggaggagg tggcacgggt 1560
aaaggaacag ctggccttcc agatggagca agcgaagcgt gagtctgaga tgaagatgga 1620
agagcagagc gaccagtggg agaagctcaa gagggagctg gcggccaggg caggagagct 1680
ggcccgctgcg caggaggccc tgagccgcac agaacagagt gggtcagagc tgagctcacg 1740
gtgggacaca ctgaacgcgg agaaggaagc cctgagtggg gtcgttcggc agcgtgaggc 1800
agagctgctg gccgctcaga gcctggtgcg ggagaaggag gaggcgctta gccaagagca 1860
gcagcggagc tcccaggaga agggcgagct acgggggcag ctggcagaaa aggagtctca 1920
ggagcagggg cttcggcaga agctgctgga tgagcagttg gcggtgttgc gaagtgcagc 1980
cgccgaggca gaggccatcc tacaggatgc agtgagcaag ctggacgacc ccctgcacct 2040
ccgctgcacc agtccccag actacttggt gagccgggct caggcagccc tggacagcgt 2100
gagcggcctg gagcagggcc acaccagta cctggcttcc tccgaagatg cttctgcct 2160
ggtggcagcg ctgacctgct tctcccattt ggctgcggac accattgtca atggtgccgc 2220
cacctccac ctggccccc cccgacccgc cgaccgcctg atggacacat gcaggagtg 2280
tggagccccg gctctggagc tgggtgggaca gctgcaagac cagacagtgc tacggagggc 2340
tcagcccagc ctgatgcggg ccccccctga gggcattctg cagttgggcc aggacttgaa 2400
gcctaagagc ctggatgtac ggcaagagga gctaggggcc atggtggaca aggagatggc 2460
ggccacctcg gcagccattg aggacgctgt gcggaggatc gaggacatga tgagccaggc 2520
ccgccacgag agctcaggcg tgaactgga ggtgaatgag aggatcctca actcctgcac 2580
agacctgatg aaggcttatcc ggctcctggt gatgacctcc accagcctgc agaaggaaat 2640
tgtggagagc ggcagggggg cagcaacgca gcaggaaatt tatgccaaga attcacgggtg 2700
gactgaaggc ctcatctcag cctctaaggc agtgggctgg ggagccacac agctggtgga 2760
gtcagctgac aaggttgtgc ttcacatggg caaatacgag gaactcatcg tctgctccca 2820
tgagattgag gccagcacgg cccagctggt ggcagcctcg aaggtgaaag ccaacaagaa 2880
cagtccccac ttgagccgcc tgcaggaatg ttcccgcaat gtcaacgaga gggctgccaa 2940
cgctgtggcc tccaccaaat ctggccagga gcagattgag gacagagaca ccatggattt 3000
ctctggcctg tccctcatca agttgaagaa gcaggagatg gagacacagg tgcgagtctt 3060
ggagctggag aagacactag aggcagagcg tgtccggctc ggggagcttc ggaaacagca 3120
ctatgtactg gctgggggga tgggaacacc tagcgaagaa gaaccagca gaccagccc 3180
agctccccga agtggggcca ctaagaagcc accgctggcc cagaaaccca gcatagcccc 3240
caggacagac aaccagctcg acaaaaagga tgggtgtctac ccagctcaac ttgtgaacta 3300
ctaggccctc aaggtgttca gcaggatggc tgggtggtgt gcctgggctt catgtggctg 3360
tctggcagtg gtcaaggggc ctctgagaag cctccaactc ctgcccaggg ggcctagtct 3420
gtgggacagt tcatctggat gtgaatctat ttatcttaag taggaactgc ctcgagcagc 3480
tgggaccag caggcctgag ccacaaatct gcagcgagca tcagagatag tctgaatgct 3540
gcgaggtatt tctttcttcg taagtttagt cagcacactg ggaaaaggct acataagcca 3600
ggagcctcct tgtctctgga ctcaaaagtc tgaggcctta agtgaacaac agaaagaggg 3660
tccctgctgg ctaccaggga taaggggatg acctgtgacc cttgagccag ggagagcagg 3720
taagctgggt ggtgtcatca cctgggggcc tgggtgctagg gcatccatgc tgggagcccc 3780
aggagaccag gctttgtgtg ggagcctggc atcatogtgg ctggggcagc ccctgctcag 3840
gtgctgtctc tgcccgtagc cttgaagcca cctccccccc gtacagtttt ccattctcct 3900
ggctactagt gtggctgttc attgcctacc ttgatgagta gatttcagcc ctccctaaagc 3960
tggggccttt cctcgtgcc 3979

```

<210> 11
 <211> 1068
 <212> PRT
 <213> Mouse

<400> 11
 Met Asn Ser Ile Lys Asn Val Pro Ala Arg Val Leu Ser Arg Arg Pro
 1 5 10 15
 Gly His Ser Leu Glu Ala Glu Arg Glu Gln Phe Asp Lys Thr Gln Ala
 20 25 30

```

Ile Ser Ile Ser Lys Ala Ile Asn Ser Gln Glu Ala Pro Val Lys Glu
35 40 45
Lys His 50 Ala Arg Arg Ile Ile Leu Gly Thr His His Glu Lys Gly Ala
55 60
Phe Thr Phe Trp Ser Tyr Ala Ile Gly Leu Pro Leu Ser Ser Ser Ser
65 70 75 80
Ile Leu Ser Trp Lys Phe Cys His Val Leu His Lys Val Leu Arg Asp
85 90 95
Gly His Pro Asn Val Leu His Asp Tyr Gln Arg Tyr Arg Ser Asn Ile
100 105 110
Arg Glu Ile Gly Asp Leu Trp Gly His Leu Arg Asp Gln Tyr Gly His
115 120 125
Leu Val Asn Ile Tyr Thr Lys Leu Leu Thr Lys Ile Ser Phe His
130 135 140
Leu Lys His Pro Gln Phe Pro Ala Gly Leu Glu Val Thr Asp Glu Val
145 150 155 160
Leu Glu Lys Ala Ala Gly Thr Asp Val Asn Asn Ile Phe Gln Leu Thr
165 170 175
Val Glu Met Phe Asp Tyr Met Asp Cys Glu Leu Lys Leu Ser Glu Ser
180 185 190
Val Phe Arg Gln Leu Asn Thr Ala Ile Ala Val Ser Gln Met Ser Ser
195 200 205
Gly Gln Cys Arg Leu Ala Pro Leu Ile Gln Val Ile Gln Asp Cys Ser
210 215 220
His Leu Tyr His Tyr Thr Val Lys Leu Met Phe Lys Leu His Ser Cys
225 230 235 240
Leu Pro Ala Asp Thr Leu Gln Gly His Arg Asp Arg Phe His Glu Gln
245 250 255
Phe His Ser Leu Lys Asn Phe Phe Arg Arg Ala Ser Asp Met Leu Tyr
260 265 270
Phe Lys Arg Leu Ile Gln Ile Pro Arg Leu Pro Glu Gly Pro Pro Asn
275 280 285
Phe Leu Arg Ala Ser Ala Leu Ala Glu His Ile Lys Pro Val Val Val
290 295 300
Ile Pro Glu Glu Ala Pro Glu Glu Glu Pro Glu Asn Leu Ile Glu
305 310 315 320
Ile Ser Ser Ala Pro Pro Ala Gly Glu Pro Val Val Val Ala Asp Leu
325 330 335
Phe Asp Gln Thr Phe Gly Pro Pro Asn Gly Ser Met Lys Asp Asp Arg
340 345 350
Asp Leu Gln Ile Glu Asn Leu Lys Arg Glu Val Glu Thr Leu Arg Ala
355 360 365
Glu Leu Glu Lys Ile Lys Met Glu Ala Gln Arg Tyr Ile Ser Gln Leu
370 375 380
Lys Gly Gln Val Asn Gly Leu Glu Ala Glu Leu Glu Gln Arg Lys
385 390 395 400
Gln Lys Gln Lys Ala Leu Val Asp Asn Glu Gln Leu Arg His Glu Leu
405 410 415
Ala Gln Leu Lys Ala Leu Gln Leu Glu Gly Ala Arg Asn Gln Gly Leu
420 425 430
Arg Glu Glu Ala Glu Arg Lys Ala Ser Ala Thr Glu Ala Arg Tyr Ser
435 440 445
Lys Leu Lys Glu Lys His Ser Glu Leu Ile Asn Thr His Ala Glu Leu
450 455 460
Leu Arg Lys Asn Ala Asp Thr Ala Lys Gln Leu Thr Val Thr Gln Gln
465 470 475 480
Ser Gln Glu Glu Val Ala Arg Val Lys Glu Gln Leu Ala Phe Gln Met
485 490 495
Glu Gln Ala Lys Arg Glu Ser Glu Met Lys Met Glu Glu Gln Ser Asp
500 505 510
Gln Leu Glu Lys Leu Lys Arg Glu Leu Ala Ala Arg Ala Gly Glu Leu
515 520 525

```

Ala	Arg	Ala	Gln	Glu	Ala	Leu	Ser	Arg	Thr	Glu	Gln	Ser	Gly	Ser	Glu
530						535					540				
Leu	Ser	Ser	Arg	Leu	Asp	Thr	Leu	Asn	Ala	Glu	Lys	Glu	Ala	Leu	Ser
545					550					555					560
Gly	Val	Val	Arg	Gln	Arg	Glu	Ala	Glu	Leu	Leu	Ala	Ala	Gln	Ser	Leu
				565						570					575
Val	Arg	Glu	Lys	Glu	Glu	Ala	Leu	Ser	Gln	Glu	Gln	Gln	Arg	Ser	Ser
			580					585					590		
Gln	Glu	Lys	Gly	Glu	Leu	Arg	Gly	Gln	Leu	Ala	Glu	Lys	Glu	Ser	Gln
		595					600					605			
Glu	Gln	Gly	Leu	Arg	Gln	Lys	Leu	Leu	Asp	Glu	Gln	Leu	Ala	Val	Leu
610						615					620				
Arg	Ser	Ala	Ala	Ala	Glu	Ala	Glu	Ala	Ile	Leu	Gln	Asp	Ala	Val	Ser
625					630					635					640
Lys	Leu	Asp	Asp	Pro	Leu	His	Leu	Arg	Cys	Thr	Ser	Ser	Pro	Asp	Tyr
				645					650					655	
Leu	Val	Ser	Arg	Ala	Gln	Ala	Ala	Leu	Asp	Ser	Val	Ser	Gly	Leu	Glu
			660					665					670		
Gln	Gly	His	Thr	Gln	Tyr	Leu	Ala	Ser	Ser	Glu	Asp	Ala	Ser	Ala	Leu
		675					680					685			
Val	Ala	Ala	Leu	Thr	Arg	Phe	Ser	His	Leu	Ala	Ala	Asp	Thr	Ile	Val
690						695					700				
Asn	Gly	Ala	Ala	Thr	Ser	His	Leu	Ala	Pro	Thr	Asp	Pro	Ala	Asp	Arg
705					710					715					720
Leu	Met	Asp	Thr	Cys	Arg	Glu	Cys	Gly	Ala	Arg	Ala	Leu	Glu	Leu	Val
				725					730					735	
Gly	Gln	Leu	Gln	Asp	Gln	Thr	Val	Leu	Arg	Arg	Ala	Gln	Pro	Ser	Leu
			740					745					750		
Met	Arg	Ala	Pro	Leu	Gln	Gly	Ile	Leu	Gln	Leu	Gly	Gln	Asp	Leu	Lys
		755				760					765				
Pro	Lys	Ser	Leu	Asp	Val	Arg	Gln	Glu	Glu	Leu	Gly	Ala	Met	Val	Asp
		770				775					780				
Lys	Glu	Met	Ala	Ala	Thr	Ser	Ala	Ala	Ile	Glu	Asp	Ala	Val	Arg	Arg
785					790					795					800
Ile	Glu	Asp	Met	Met	Ser	Gln	Ala	Arg	His	Glu	Ser	Ser	Gly	Val	Lys
				805					810					815	
Leu	Glu	Val	Asn	Glu	Arg	Ile	Leu	Asn	Ser	Cys	Thr	Asp	Leu	Met	Lys
			820					825					830		
Ala	Ile	Arg	Leu	Leu	Val	Met	Thr	Ser	Thr	Ser	Leu	Gln	Lys	Glu	Ile
		835					840					845			
Val	Glu	Ser	Gly	Arg	Gly	Ala	Ala	Thr	Gln	Gln	Glu	Phe	Tyr	Ala	Lys
		850				855					860				
Asn	Ser	Arg	Trp	Thr	Glu	Gly	Leu	Ile	Ser	Ala	Ser	Lys	Ala	Val	Gly
865					870					875					880
Trp	Gly	Ala	Thr	Gln	Leu	Val	Glu	Ser	Ala	Asp	Lys	Val	Val	Leu	His
				885					890					895	
Met	Gly	Lys	Tyr	Glu	Glu	Leu	Ile	Val	Cys	Ser	His	Glu	Ile	Ala	Ala
			900					905					910		
Ser	Thr	Ala	Gln	Leu	Val	Ala	Ala	Ser	Lys	Val	Lys	Ala	Asn	Lys	Asn
		915					920					925			
Ser	Pro	His	Leu	Ser	Arg	Leu	Gln	Glu	Cys	Ser	Arg	Thr	Val	Asn	Glu
		930				935					940				
Arg	Ala	Ala	Asn	Val	Val	Ala	Ser	Thr	Lys	Ser	Gly	Gln	Glu	Gln	Ile
945					950					955					960
Glu	Asp	Arg	Asp	Thr	Met	Asp	Phe	Ser	Gly	Leu	Ser	Leu	Ile	Lys	Leu
				965					970					975	
Lys	Lys	Gln	Glu	Met	Glu	Thr	Gln	Val	Arg	Val	Leu	Glu	Leu	Glu	Lys
			980					985					990		
Thr	Leu	Glu	Ala	Glu	Arg	Val	Arg	Leu	Gly	Glu	Leu	Arg	Lys	Gln	His
		995					1000					1005			
Tyr	Val	Leu	Ala	Gly	Gly	Met	Gly	Thr	Pro	Ser	Glu	Glu	Glu	Pro	Ser
	1010					1015						1020			

Arg Pro Ser Pro Ala Pro Arg Ser Gly Ala Thr Lys Lys Pro Pro Leu
 1025 1030 1035 1040
 Ala Gln Lys Pro Ser Ile Ala Pro Arg Thr Asp Asn Gln Leu Asp Lys
 1045 1050 1055
 Lys Asp Gly Val Tyr Pro Ala Gln Leu Val Asn Tyr
 1060 1065

<210> 12
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> sequencing primer

<400> 12
 gaagataccc caccaaac 18

<210> 13
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> cDNA primer

<400> 13
 gcttgacagt gtagtcataa aggtggctgc agtcc 35

<210> 14
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 14
 ggacatgtcc agggagttga atac 24

<210> 15
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 15
 cuacuacuac uacuaggcca cgcgtcgact agtacggggg ggggg 45

<210> 16
 <211> 516
 <212> DNA
 <213> Human

<400> 16
 tctgtggaag gtttgaggag gagagagggg cagctggatg ctcttgggccc acggtcgccc 60
 ctgatctctg cgctcttcc tcctgctocg ggagaaataa tgttccctg ggggatgaaa 120
 gcatctcttt gtgcgggctt taattgccat gttgtgtgac caagggagtg agtggcgccg 180
 ggaccagcag ctgggcacag ccaatgccag gcagtgggtg cactccctc aggacgccc 240
 gccagctggc tcctgggagc gctgcccacc tctgccccca gctgggcgccc tgcaaggaac 300

cgaccacccg	tggggctggg	ggaggttggc	tggaggagga	gaaaggggag	ggctctggga	360
gggtctcagc	cactctcaga	ggcttattca	tctcatcctc	ctttccctcc	cccttcttgt	420
ttttcagact	gtcagcatca	ataaggccat	taatacgcag	gaagtggctg	taaaggaaaa	480
acacgccaga	aatatccttt	ggatgttgct	tggaaag			516

<210> 17
 <211> 193
 <212> DNA
 <213> Human

<400> 17						
tgttttccat	aacccccctt	caccgtgcat	actgggcacc	caccatgaga	aaggggcaca	60
gaccttctgg	tctgttggtc	accgcctgcc	tctgtctagc	aaccagtgcc	tctgctggaa	120
gtttctgcat	gtgttccaca	aactcctccg	agatggacac	ccgaacgtga	gttcctgggg	180
ctatgggggtg	gca					193

<210> 18
 <211> 104
 <212> DNA
 <213> Human

<400> 18						
gtgttctttt	gcccctgcag	gtcctgaagg	actctctgag	atacagaaat	gaattgagtg	60
acatgagcag	gatgtgggtg	agtttggaga	tgtactcagg	agcc		104

<210> 19
 <211> 327
 <212> DNA
 <213> Human

<400> 19						
aattcctggc	tgcagatctc	ttgactgtta	tgttcttggt	gttgactctg	tttccctccc	60
tcttccctaaa	agggccacct	gagcgagggg	tatggccagc	tgtgcagcat	ctacctgaaa	120
ctgctaagaa	ccaagatgga	gtaccacacc	aaagtgagtc	tctgcggaca	gttctgccgc	180
caccgcccgc	tcccctgctc	catcccttca	gcccctccct	gggctcattt	gtcagctctt	240
tcaggtaata	gacagcccag	gcttctgagg	aagtgtgcac	atcatgtacc	caagctgtga	300
gagaggaaaag	ccaccgccag	gcccacg				327

<210> 20
 <211> 331
 <212> DNA
 <213> Human

<400> 20						
gggtctcaagc	aatcctccca	cctcggcctc	ccaagtagct	gggaccacag	gcgtgtgcc	60
ccacgcccgg	ctgagagagg	gctcttcatg	tcttctgccc	tgactccctt	cctctgcctc	120
ccttccagaa	tcccaggttc	ccaggcaacc	tgcagatgag	tgaccgccag	ctggacgagg	180
ctggagaaaag	tgacgtgaac	aacttgtaag	tggctcctgc	cctgagccca	gggagggaga	240
aagcttttgt	gaatgctgac	acttctcata	agggctatgg	agggcctgat	ggggggaggc	300
cgtggctggg	atggggacca	aagcccctgg	g			331

<210> 21
 <211> 470
 <212> DNA
 <213> Human

<400> 21						
actgtcgctg	tcactgttga	cttcaccagg	ctgcatggcc	ataataccca	caaggctaag	60
acttgagact	ggagttgtgt	gtgtgtttgc	gcattgcacat	gagcattgga	gactggagta	120
gcgtagagcg	tgggggaggg	gacaggtaac	agaccggcct	caggctgtgg	agtgtgaagct	180
ctctttcctc	ttgggtccag	tttccagtta	acagtggaga	tgtttgacta	cctggagtg	240
gaactcaacc	tcttccaaac	aggtgagtct	cttccctccc	gtctaacc	ggctctcatg	300

ggaactacct	aattcctagt	cctcctctcc	ctgcaaagtg	tgcagcacia	ggggtaggaa	360
aatggagaca	ttcacacccc	atctctggtc	tctccaaccc	tcgtgcaggg	agggactgaa	420
cctcttcagt	atctttcttt	ttaagagaca	aggtctcggc	cgggtgcagt		470

<210> 22
 <211> 565
 <212> DNA
 <213> Human

<400> 22						
tcttcacctg	tttaatgggg	atacgtttac	ctatctcatg	ggagtgttgt	gaaggttaaa	60
tgaattagat	gaggtaaagc	acgcacagaa	tcggtccttg	gtgtatgttg	gacccctgcc	120
tctgcccctc	tgaagaggct	gcctgtaatc	ccctggctct	accaccttcc	tccctcactt	180
ttatttccta	gtattcaact	ccctggacat	gtcccgtct	gtgtccgtga	cggcagcagg	240
gcagtgccgc	ctcgccccgc	tgatccaggt	catcttggac	tgcagccacc	tttatgacta	300
cactgtcaag	cttctcttca	aactccactc	ctgtgagtac	cgcgggccag	atcttcttac	360
atgagattca	ggccagaggg	aggatcccag	cctgaggatg	tccccagaga	aacgcagtc	420
ttctcagtgc	ctttggctgt	ctgcttctgt	tccaaaaggg	cccggagctt	ctgaccattg	480
tgaggataaa	agagcagggc	ccaggctttg	gtgaccccag	taaagcccct	ggcttgccac	540
tcttgcgctc	agtgttacag	gatct				565

<210> 23
 <211> 233
 <212> DNA
 <213> Human

<400> 23						
gggacagctc	taggccagtc	gtggcccctg	gcagtgtctg	ccacatgccc	cagggtagct	60
gggcccctcc	ccctcgagag	ccccgctgtg	gcttcccctg	cctctggtcc	ccctcccctc	120
tcacactctt	tccaatttct	tccaggcctc	ccagctgaca	ccctgcaagg	ccaccgggac	180
cgcttcatgg	agcagtttac	aaagtaagtg	gttcaagtaa	caggaatgga	ggt	233

<210> 24
 <211> 578
 <212> DNA
 <213> Human

<400> 24						
tgaatcccag	caccatggag	tttatctcct	tgacagcctg	tgcctttggg	ctggggaggg	60
ggcaggaag	ccaggtggct	gctctgtccc	ctacatgggg	ctgatgaaga	cacccagcac	120
ccctcaggtc	cttctccacc	cctaggttga	aagatctgtt	ctaccgctcc	agcaacctgc	180
agtaactcaa	gcggtcatt	cagatccccc	agctgcctga	ggtaagcatg	cccaaccaca	240
caccctcggc	actgcagagg	ccccaggtac	tctcttaagg	gccggcgggg	cctggcaagc	300
aagcactatt	tgaggatgtg	tctccgtctt	cagaacccac	ccaacttctt	gcgagcctca	360
gccctgtcag	aacatatcag	ccctgtgggt	gtgatccctg	cagaggcctc	atcccccgac	420
agcgagccag	tcctagagaa	ggatgacctc	atggacatgg	atgcctctca	gcaggtgagg	480
accacttggg	agagaaactt	ggcctttcct	ctcacctgca	agtacagggg	agaggctggg	540
ggagaccctg	gccaaagccc	attgactcta	accaggtt			578

<210> 25
 <211> 390
 <212> DNA
 <213> Human

<400> 25						
aaaaaaattt	aaaaaattaa	acaggtctga	accgtttaat	tcgagaaagg	gggcattctc	60
ccatatcact	caactgaccc	acacacagaa	ttctctggct	ctctgactta	ttctcactcc	120
ttttttgtga	accacagaat	ttatttgaca	acaagtttga	tgacatcttt	ggcagttcat	180
tcagcagtga	tccttccaat	ttcaacagtc	aaaatgggtg	gaacaaggat	gagaagtgag	240
tccaagctgg	gttcaagcag	atggttcagg	agctaagtta	agccatgggc	tgcttcaaaa	300
cactaaccaa	agaggaaatt	ttaatgatac	tggggcttct	tagatacaga	acatcttgaa	360
gggttggggg	caatggctta	tgctgtaat				390

<210> 26
 <211> 547
 <212> DNA
 <213> Human

<400> 26
 aaaatcaata accatggatt tatgagtatt agattagtat ctggtaacat ttagagtata 60
 atttatggca tttcaaagaa ttgtccccc aaattaacca gcttttaatt tcctcccctg 120
 agctcacaat taaaaacaga gggatagaag cactatgaaa gcaaaactcat tccccttctc 180
 ttcccaggga ccacttaatt gagcgactat acagagagat cagtggattg aaggcacagc 240
 tagaaaacat gaagactgag gtataaacttg gatctgctct gcctttgctc ttcacaaaaa 300
 cacggtagat ttgaatgtta aatttgcac acactagcca ggcacagtgg ctcacacctg 360
 taatcctagc actttgggag gccaaaggcag gaggattacc tgaggtcggg agttcgagac 420
 cagcctgggc aacaggggtga aacccccgtc ttcaataaaa atgcaataat tagccgggtg 480
 tgttggcagg cacctgtaat cccagctact cgggaagctg aggcattgaga attgcttgaa 540
 cttggga 547

<210> 27
 <211> 436
 <212> DNA
 <213> Human

<400> 27
 cccccagcca ctctaaagag gaccacaatt ccccgcccat catcccctgt tattgttgtt 60
 gattgagggg ctcctaataa ccagatggtc caaccctcct gggacgtgga gagttgactt 120
 aggggaatca ggtatttact tggaagcatg gtaggaccgc cttctccggc ccatgcccgt 180
 gaccctgtgc agtgggctgt tggcctcatg accggagtc cccacagag ccagcgggtt 240
 gtgctgcagc tgaagggccg cgtcagcgag ctggaagcag atctggccga gcagcagcac 300
 ctgcccgcagc agggcgccga cgactgtgaa ttcttgccgg cagaactgga cgagctcagg 360
 aggcagcggg aggcacccga gaaggctcag cggagcctgt ctgagataga aagtgagcgg 420
 tgggtggggg cggggg 436

<210> 28
 <211> 469
 <212> DNA
 <213> Human

<400> 28
 gacttgagcc caaggaggtc aaggctgcag tgaacagtga ttgtgccact gcaccccagc 60
 ctgggtgaca gagcaagact gtctcaaaac aaaacaagga ggaccttcta gggaccctgg 120
 ctcatcgcaa ggaaggcaag ggtccctgct aggttagact cctcaccttg gtcctttaca 180
 atacagggaa agctcaagcc aatgaacagc gatatagcaa gctaaaggag aagtacagcg 240
 agctggttca gaaccacgct gacctgctgc ggaaggtaag accctcagcc cctgtcacca 300
 tcctgcaggg cctgcacctc tagggagaga gcgctcagg cctgtggctt ccccggggac 360
 agcaaccctt acattgatct ctaaggcatt gccgtcatct cgggaaccac accttttcag 420
 gcttccttgc ctctgtgtct tgggctgtgt cctgggtgac aatcccatg 469

<210> 29
 <211> 359
 <212> DNA
 <213> Human

<400> 29
 gggtagga aa gtgattcctg tgtctgactc tagggcagc acagcctgag tatgattgtc 60
 ctagaaggag gatgtcctct aagcctggga tctcctgggt caagacactg ttcttctttt 120
 gcagaatgca gaggtgacca aacaggtgtc catggccaga caagcccagg tagatttgga 180
 acgagagaaa aaagagctgg aggttcggt ggagcgcatc agtgaccagg gccagcggaa 240
 ggtgagtggg acgaggagca ctcgggaaat gagggagggg gctgttgagt tgggtggcgg 300
 ggctttgtgg ccttctgctc catgggcagt tctgtgggtc ggttggcatc acacagcag 359

<210> 30

<211> 209
 <212> DNA
 <213> Human

<400> 30							
gttgatcgct	tgaggacgttt	ttacattttt	atattctttg	tactgtcac	ccagatcaga		60
gtccctctgt	ttttcttctc	tttcagactc	aagaacagct	ggaagtctta	gagagcttga		120
agcaggaact	tgccacaagc	caacgggagc	ttcaggttct	gcaaggcagc	ctggaaactt		180
ctgcccaggt	aaatacctcc	ttttttttt					209

<210> 31
 <211> 485
 <212> DNA
 <213> Human

<400> 31							
ccccactgc	aatcagtgtg	tccccgggag	ggaatcagag	tggcaggtta	aagagccatc		60
accttcccag	tccttgcaac	ccggtggtgg	gttggaacctc	tggaagtag	ggactgttta		120
actcaaccag	cgtctccctc	tttccttgtg	gtcacctttg	cagtcagaag	caaactgggc		180
agccgagttc	gccgagctag	agaaggagcg	ggacagcctg	gtgagtggcg	cagctcatag		240
ggaggaggaa	ttatctgctc	ttcggaaga	actgcaggac	actcagctca	aactggccag		300
cacagagggt	cacggacatg	gacacgagcg	agcacctgtg	aattcccacc	gagggcctct		360
gcgcattgcac	ggaggctggg	aggaccccgg	ggctgctgag	aaggggtttg	gggccttggc		420
ctgattgtgc	agacattctg	taggtgtaat	gccagcaggc	cctgcattgc	ctgcagagtc		480
catga							485

<210> 32
 <211> 468
 <212> DNA
 <213> Human

<400> 32							
ttactggcct	ggacctcatt	ggccatgact	tgagctaaga	tgctaagagc	cccagccagg		60
tcactcctgt	caggttcatt	atggagtcta	gggcagactc	tcacctccct	ggaccatttt		120
tagaatctat	gtgccagctt	gccaagacc	aacgaaaaat	gcttctgggtg	gggtccagga		180
aggctgcgga	gcaggtgata	caagacgccc	tgaaccagct	tgaagaacct	cctctcatca		240
gctgcgctgg	gtctgcaggt	acacttgcaa	ttgccagct	ggcaggggcc	aggtccttac		300
agcctgagac	tctgttgatg	ttgaatctca	tgtgagactt	agctcagggg	ctctcagccc		360
agcagcatgt	cagcattacc	ttagggggcg	ccaggcccca	tcctagatca	gttacatgtg		420
gaaactctgt	gcattagtcg	ctatacacta	gtatttttagt	atcttctt			468

<210> 33
 <211> 393
 <212> DNA
 <213> Human

<400> 33							
cactagtaag	ctcctccatt	cagtgtctta	ttaacgagga	tgaagccagc	tatgagaact		60
tgctctgacc	ttgcctgtg	ttcctctca	cagatcacct	cctctccacg	gtcacatcca		120
tttccagctg	catcgagcaa	ctggagaaaa	gctggagcca	gtatctggcc	tgcccagaag		180
gtaagaatgg	ccaaggacag	tctctgtcgg	ctagtgtatg	ccagacaggg	ttcagaagca		240
cctgaatcgg	gggatagtga	caggtccctc	tgcatcaaga	aaggcatgta	ggcaactcat		300
acaagaaagg	catgtaggca	actcataaaa	cgggaggaga	gggtatgaaa	gtgtcaccat		360
caaccagacc	tgagaaactt	ctctttccaa	tcc				393

<210> 34
 <211> 421
 <212> DNA
 <213> Human

<400> 34							
ggcctgccca	gaaggtaaga	atggccaagg	acagtctctg	tcggctagtg	atggccagac		60

aggggttcaga	agcacctgaa	tgcgggggata	gtgacagggtc	cctctgcatac	aagaaaggca	120
tgtaggcaac	tcatacaaga	aaggcatgta	ggcaactcat	aaaacgggag	gagaggggtat	180
gaaagtgtca	ccatcaacca	gacctgagaa	acttctcttt	ccaatcctgg	cagacatcag	240
tggacttctc	cattccataa	ccctgctggc	ccacttgacc	agcgacgcca	ttgctcatgg	300
tgccaccacc	tgcctcagag	ccccacctga	gcctgccgac	tgtgagtact	ggggcatgag	360
gggctgttca	tggaccaggg	gagcaggggg	cctttaaag	tctctgttgg	gccgggcgca	420
g						421

<210> 35
 <211> 498
 <212> DNA
 <213> Human

<400> 35						
aggccgagggc	aggagaatcg	cttgaactca	ggaggcggag	tttgagtgta	gccgagatgg	60
cgccactgca	ctccagcctg	ggcaacaaga	gcgagactcc	atctcaaaaa	aaaagtgtct	120
attgccttgt	atctccagca	ctgaccgagg	cctgtaagca	gtatggcagg	gaaaccctcg	180
cctacctggc	ctccctggag	gaagagggaa	gccttgagaa	tgccgacagc	acagccatga	240
ggaactgcct	gagcaagatc	aaggccatcg	gcgaggtact	tggagtagta	tcattgagga	300
gcattgttat	tcttctgggt	gtgcgtgctg	gtgaatggcc	agggaaatcg	tgatgttctg	360
agctagttct	ttctgcactt	agaacttgat	tctagaaaga	gattgttaaa	attggaaaat	420
ctggccgggt	gcagtgattt	atgcgtgtaa	tcccagcact	ttgggaggcc	gagtcaggag	480
gatcacttga	ggctagac					498

<210> 36
 <211> 427
 <212> DNA
 <213> Human

<400> 36						
ccctgtggct	tgcagaaggt	gtttgctggg	tggcctcctg	ccttgccatc	ttgtaagggt	60
tacagatggc	agaggagaag	agacaggagg	ccccaagggtc	agttcagcct	ttgtgatgtg	120
ttcacaggag	ctcctgcccc	ggggactgga	catcaagcag	gaggagctgg	gggacctggt	180
ggacaaggag	atggcggcca	cttcagctgc	tattgaaact	gccacggcca	gaatagaggt	240
aggaggttcc	tgcaggatct	cctgaaacga	tgcctttgca	gctgcccttc	tgcaacactg	300
ctcattaaac	atgtcacagt	cgttcattaa	ggccatggca	accccctaag	acagaaacca	360
gaatttgcca	ggcacagtgg	ctcatgcctg	taaccccagc	accttggggag	gatcacttga	420
gtccagg						427

<210> 37
 <211> 367
 <212> DNA
 <213> Human

<400> 37						
ccccctgaat	aggtttagagt	ctggattctt	ttctgactct	ctcaagaatg	tgggcaggga	60
cttggggact	tccagattca	ggtttcccag	ctaccacacg	atgttggact	gaaagtatag	120
taagacatta	gtggatcctt	aatattcaag	gcacatttag	aaaccatgct	tctttttcac	180
aggagatgct	cagcaaattc	cgagcaggag	acacaggagt	caaattggag	gtgaatgaaa	240
ggtcgggtctg	agcggcatgg	tgggacctag	gggagcagga	tctgtcttcc	tgacattggt	300
ctatactttg	catacttatt	agggaattag	aggagagcag	tagcagccac	ggggaagggc	360
tgagttg						367

<210> 38
 <211> 502
 <212> DNA
 <213> Human

<400> 38						
ccccgcagaa	tgttccagca	acctcagcac	ccttcttacc	tccctttccc	attccaagct	60
tgcctttggc	taggagtggg	gaagagaacc	gtcgtgttca	ttgatcttgg	atcttgatct	120
cagtgtatcc	tgcacttggt	tgtttggcag	gatccttggt	tgctgtacca	gcctcatgca	180

agctattcag	gtgctcatcg	tggcctctaa	ggacctccag	agagagattg	tgagagacgg	240
cagggtgagc	gtgggtgtgg	gccctgggca	ggaagaggag	gcaccggtga	cagactcccc	300
ctccaacgga	ctctgtgatg	ctgccgtctt	actctgtgtg	tcacactgag	tacagagcag	360
ccactcctgt	agatatcagc	agaggccctg	gggagaagtc	agagctccag	gacctcccca	420
gagggtggcc	aggcatgtgt	cccaactcca	gctcccttcg	cacaggcaga	cattgttgga	480
acttgctgtg	ggagcccttt	tt				502

<210> 39
 <211> 437
 <212> DNA
 <213> Human

<400> 39						
ttttggtctc	tgaatcttct	tcttttttgt	aaaatgggaa	tactaatgct	tatgtctcag	60
agttactatg	aggatgattt	gggataatat	atgtataaaa	gcacctgcc	tatagtacat	120
gctcaataaa	aggtggctat	tactattttt	tatttcctta	gggtacagca	tcccctaaag	180
agttttatgc	caagaactct	cgatggacag	aaggacttat	ctcagcctcc	aaggctgtgg	240
gctggggagc	cactgtcatg	gtgtaagtat	ctattgggtac	caagggtcct	cccatgacct	300
ctcttccatt	gatccactcc	aaacaatagc	taaggaggga	aaaaaaaaatc	tgtcccttag	360
aaataaacta	ttgatcagga	agtcaatagg	accgagttta	caaggagacc	tggtctctcc	420
aggggacaca	gggcagg					437

<210> 40
 <211> 351
 <212> DNA
 <213> Human

<400> 40						
gggagcctgg	ctctcccagg	ggacacaggg	caggcagcct	cccctccctg	tttagccaag	60
ggcgatgggg	tggtctggag	gtgggattgt	ggaggagtgt	cagctcattt	gcccgttaacc	120
tagtccctct	tgctgttttc	catcagggat	gcagctgac	tggtgtgaca	aggcagaggg	180
aaatttgagg	agctaattgt	gtgttctcat	gaaattgtctg	ctagcacagc	ccagcttgtg	240
gctgcatcca	aggtaggacc	tggtctggacc	tcctaggacg	ctggaaggcc	tggttagaga	300
gtactaggct	aggttaaaga	gtacttggct	gcgttaggca	gtacttggct	g	351

<210> 41
 <211> 418
 <212> DNA
 <213> Human

<400> 41						
ctttttatat	gatagatatg	tcaggagctg	actatagtca	gcagattttg	agaagctgat	60
tggtgattgc	cgtttggccc	acatatgttt	gctaagaacc	atcagagcaa	ttatctgatt	120
cagtccttgt	tgctctaggt	gttgatatga	cctaactctg	ctttgtcctg	gtaggtgaaa	180
gctgataagg	acagccccc	cctagcccag	ctgcagcagg	cctctcgggg	agtgaaccag	240
gccactgccg	gcgttgtggc	ctcaaccatt	tcgggcaaat	cacagatcga	agagacaggt	300
agcctttcca	aaggggacct	tttcttacc	accctgttga	gctcttctct	gcacctctcc	360
ctgtgatccc	aaccaaattc	cacaggactg	tgtctaaatt	ctttcatatt	tttcatct	418

<210> 42
 <211> 279
 <212> DNA
 <213> Human

<400> 42						
tttccacaga	gcattggcat	tggtgcctc	tcaggtgcca	gtcagccagg	gtagaatttg	60
atgagacctt	cttgtttcca	tccttgccga	caacatggac	ttctcaagca	tgacgctgac	120
acagatcaaa	cgccaagaga	tggtattctca	ggttagggtg	ctagagctag	aaaatgaatt	180
gcagaaggag	cgtcaaaaac	tggtgagagct	tcggaaaaag	cactacgagc	ttgctgggtg	240
tgctgagggc	tggtgaagaag	gtaagctgac	tcaaaggat			279

<210> 43

<211> 3715
 <212> DNA
 <213> Human

<400> 43

aacataaatt	atcattgtct	tttaggaaca	gaggcatctc	cacctacact	gcaagaagtg	60
gtaaccgaaa	aagaatagag	ccaaaccaac	accccatatg	tcagtgtaaa	tccttggtac	120
ctatctcgtg	tgtgttattt	ccccagccac	aggccaaatc	cttgaggatc	caggggcagc	180
cacaccactg	ccattaccca	gtgccgagga	catgcatgac	acttcccaaa	gactccctcc	240
atagcgacac	cctttctgtt	tggacccatg	gtcatctctg	ttcttttccc	gcctccctag	300
ttagcatcca	ggctggccag	tgctgcccat	gagcaagcct	aggtacgaag	aggggtggtg	360
gggggcaggg	ccactcaaca	gagaggacca	acatccagtc	ctgctgacta	tttgaccccc	420
acaacaatgg	gtatccttaa	tagaggagct	gcttgttgtt	tggtgacagc	ttggaaaggg	480
aagatccttat	gccttttctt	ttctgttttc	ttctcagtct	tttcagtttc	atcatttgca	540
caaacttgtg	agcatcagag	ggctgatgga	ttccaaacca	ggacactacc	ctgagatctg	600
cacagtcaga	aggacggcag	gagtgtcctg	gctgtgaatg	ccaaagccat	tctccccctc	660
tttgggcagt	gccatggatt	tccactgctt	cttatgggtg	ttggttgggt	tttttggttt	720
tgtttttttt	ttttaagttt	cactcacata	gccaaactct	ccaaagggca	cacccctggg	780
gctgagttct	cagggccccc	caactgtggt	agctccagcg	atggtgctgc	ccaggcctct	840
cggtgctcca	tctccgcctc	cacactgacc	aagtgtctgc	ccacccagtc	catgctccag	900
ggtcaggcgg	agctgctgag	tgacagcttt	cctcaaaaag	cagaaggaga	gtgagtgcct	960
ttccctccta	aagctgaatc	ccggcggaaa	gcctctgtcc	gcctttacaa	gggagaagac	1020
aacagaaaga	gggacaagag	ggttcacaca	gccaggttcc	cgtgacgagg	ctcaaaaact	1080
tgatcacatg	cctgaatgga	gctggtgaga	tcaacaacac	tacttccctg	ccggaatgaa	1140
ctgtccgtga	atggtctctg	tcaagcgggc	cgtctccctt	ggcccagaga	cggagtgtgg	1200
gagtgattcc	caactccttt	ctgcagacgt	ctgccttgge	atcctcttga	ataggaagat	1260
cgttccactt	tctacgcaat	tgacaacccc	ggaagatcag	atgcaattgc	tccatccagg	1320
gaagaacctt	atacttgggt	tgctaccctt	agtatttatt	actaacctcc	cttaagcagc	1380
aacagcctac	aaagagatgc	ttggagcaat	cagaacttca	ggtgtgactc	tagcaaagct	1440
catctttctg	cccggctaca	tcagccttca	agaatcagaa	gaaagccaag	gtgctggact	1500
gttactgact	tggatcccaa	agcaaggaga	tcatttggag	ctcttgggtc	agagaaaatg	1560
agaaaggaca	gagccagcgg	ctccaactcc	tttcagccac	atgccccagg	ctctcgctgc	1620
cctgtggaca	ggatgaggac	agagggcaca	tgaacagctt	gccagggatg	ggcagcccaa	1680
cagctacttt	cctcttctag	atggacccca	gcattttaat	gaccttctga	tcttgggaaa	1740
acagcgtctt	ccttctttat	ctatagcaac	tcatttgggt	tagccatcaa	gcacttccca	1800
ggatctgtct	caacagaata	ttgctagggt	ttgtacatg	acgggttgtg	agacttctgt	1860
ttgatcactg	tgaaccaacc	cccctctccc	tagcccaccc	ccctccccaa	ctccctctct	1920
gtgcattttc	taagtgggac	attcaaaaaa	ctctctccca	ggacctcgga	tgaccatact	1980
cagacgtgtg	acctccatac	tgggttaagg	aagtatcagc	actagaaatt	gggcagtctt	2040
aatgttgaat	gctgtcttct	gcttagtatt	tttttgattc	aaggctcaga	aggaatgggt	2100
cgtggccttc	ctgtcccagt	tgtggcaact	aaaccaaatc	gtgtgttctt	gatgcgggtc	2160
aacatttcca	aaagtggcta	gtcctcactt	ctagatctca	gccattctaa	ctcatatgtt	2220
cccaattacc	aagggttggc	cgggcacagt	ggctcacgcc	tgtaatccca	gcacttttag	2280
aggctgaggt	ggttaggatca	cctgaggtca	ggagtccaag	accagcctgt	ccaacatggt	2340
gaaaccccca	tctctactaa	aaataccaaa	aattagccga	gcgtagtgc	gggtgccctg	2400
aatcccagct	actcaggagg	ctgagacagg	agaatcacct	gaaccccaga	ggcagaggtt	2460
gcagtgaagt	gagatcacgc	cattgtactc	cagcctgggc	aacaagagca	aaactccgtc	2520
tcaaaaaaaa	aaaaaaatta	caaattggggc	aaacagtcta	gtgtaatgga	tcaaatgaag	2580
attctctgcc	cagccgggca	cagtggcgca	tgctgttaat	cccagaactt	tgggaggcca	2640
agacgggatg	attgcttgag	ctcaggaggt	tgagaccagg	ctgggcatca	tagcaagacc	2700
tcactctctac	taaaaattcaa	aaacaaaatt	agccgggcat	gatggtgcat	gcctgtagtc	2760
tcagctagt	ggggagctaa	ggtgggagaa	ttgcttgagc	ttgggaagtc	gaggctgcag	2820
tcagccctga	ttgtgccagt	gcactccggc	ctgggtgaca	gagtgcagac	cgtgctcaaa	2880
aaaaaaaaga	ttctgtgtca	gagccagacc	caggagtttg	aggtgtcaat	gagccatgat	2940
ttccactctg	actccagcct	gagtgcagca	gcgagactcc	atctctttta	aaacaaacaa	3000
aaaattatct	gaatgatcct	gtctctaaaa	agaagccaca	gaaatgttta	aaaacttcat	3060
cgacttagcc	tgagtcatata	cgggttaagaa	agcacttaaa	cagaagcaga	ggctaattca	3120
gtgtcacatg	aggaagtagc	tgctcagatg	cacataatta	ctttcgtaat	agctcagatt	3180
agaattgcta	ccccattctc	tagacaaaat	caaattgtcc	tattgtgact	cttctaaaaa	3240
tgaagatgaa	gagctattta	atgacacacc	ttggattaaa	acgggaatca	catcttaag	3300
ctaaaaatga	acctgcaagc	cttctaaatg	agtcactgag	catcactagt	gacaagctct	3360
gggtgagcgt	aaatgggtca	tgacaagatg	ggacagcaac	aaaatcatgg	cttaggatcg	3420